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SEP 08 2003

TECH CENTER 16



/600

160

## RAW SEQUENCE LISTING

DATE: 08/29/2003

PATENT APPLICATION: US/08/572,027C

TIME: 15:01:28

Input Set : A:\07148-032001.txt

Output Set: N:\CRF4\08292003\H572027C.raw

3 <110> APPLICANT: DeBonte, Lorin R.  
 4 Fan, Zhegong  
 5 Miao, Guo-Hua  
 8 <120> TITLE OF INVENTION: PLANTS HAVING MUTANT SEQUENCES THAT  
 9 CONFER ALTERED FATTY ACID PROFILES  
 11 <130> FILE REFERENCE: 07148-032001  
 13 <140> CURRENT APPLICATION NUMBER: US 08/572,027C  
 -> 14 <141> CURRENT FILING DATE: 1995-12-15  
 16 <160> NUMBER OF SEQ ID NOS: 50  
 18 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 1155  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: Brassica napus  
 25 <220> FEATURE:  
 26 <221> NAME/KEY: CDS  
 27 <222> LOCATION: (1)...(1152)  
 28 <223> OTHER INFORMATION: wild type D form  
 30 <221> NAME/KEY: misc\_feature  
 31 <222> LOCATION: 205  
 32 <223> OTHER INFORMATION: n = A,T,C or G  
 -> 34 <400> 1  
 35 atg ggt gca ggt gga aga atg caa gtg tct cct ccc tcc aag aag tct 48  
 36 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser  
 37 1 5 10 15  
 39 gaa acc gac acc atc aag cgc gta ccc tgc gag aca ccg ccc ttc act 96  
 40 Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Phe Thr  
 41 20 25 30  
 43 gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc tcg 144  
 44 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser  
 45 35 40 45  
 47 atc cct cgc tct ttc tcc tac ctc atc tgg gac atc atc ata gcc tcc 192  
 48 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser  
 49 50 55 60  
 -> 51 tgc ttc tac tac ntc gcc acc act tac ttc cct ctc ctc cct cac cct 240  
 52 Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro  
 53 65 70 75 80  
 55 ctc tcc tac ttc gcc tgg cct ctc tac tgg gcc tgc caa ggg tgc gtc 288  
 56 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val  
 57 85 90 95  
 59 cta acc ggc gtc tgg gtc ata gcc cac gaa tgc ggc cac cac gcc ttc 336  
 60 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe  
 61 100 105 110

ENTERED

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```

63 agc gac tac cag tgg ctt gac gac acc gtc ggt ctc atc ttc cac tcc      384
64 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
65      115      120      125
67 ttc ctc ctc gtc cct tac ttc tcc tgg aag tac agt cat cgc agc cac      432
68 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His
69      130      135      140
71 cat tcc aac act ggc tcc ctc gag aga gac gaa gtg ttt gtc ccc aag      480
72 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
73 145      150      155      160
75 aag aag tca gac atc aag tgg tac ggc aag tac ctc aac aac cct ttg      528
76 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
77      165      170      175
79 gga cgc acc gtg atg tta acg gtt cag ttc act ctc ggc tgg ccg ttg      576
80 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
81      180      185      190
83 tac tta gcc ttc aac gtc tcg gga aga cct tac gac ggc ggc ttc cgt      624
84 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg
85      195      200      205
87 tgc cat ttc cac ccc aac gct ccc atc tac aac gac cgc gag cgt ctc      672
88 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
89      210      215      220
91 cag ata tac atc tcc gac gct ggc atc ctc gcc gtc tgc tac ggt ctc      720
92 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
93 225      230      235      240
95 ttc cgt tac gcc gcc ggc cag gga gtg gcc tcg atg gtc tgc ttc tac      768
96 Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr
97      245      250      255
99 gga gtc ccg ctt ctg att gtc aat ggt ttc ctc gtg ttg atc act tac      816
100 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr
101      260      265      270
103 ttg cag cac acg cat cct tcc ctg cct cac tac gat tcg tcc gag tgg      864
104 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
105      275      280      285
107 gat tgg ttc agg gga gct ttg gct acc gtt gac aga gac tac gga atc      912
108 Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
109      290      295      300
111 ttg aac aag gtc ttc cac aat att acc gac acg cac gtg gcc cat cat      960
112 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
113 305      310      315      320
115 ccg ttc tcc acg atg ccg cat tat cac gcg atg gaa gct acc aag gcg      1008
116 Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
117      325      330      335
119 ata aag ccg ata ctg gga gag tat tat cag ttc gat ggg acg ccg gtg      1056
120 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
121      340      345      350
123 gtt aag gcg atg tgg agg gag gcg aag gag tgt atc tat gtg gaa ccg      1104
124 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
125      355      360      365
127 gac agg caa ggt gag aag aaa ggt gtg ttc tgg tac aac aat aag tta      1152

```

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128 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu  
 129 370 375 380

131 tga

1155

133 &lt;210&gt; SEQ ID NO: 2

134 &lt;211&gt; LENGTH: 384

135 &lt;212&gt; TYPE: PRT

136 &lt;213&gt; ORGANISM: Brassica napus

138 &lt;220&gt; FEATURE:

139 &lt;221&gt; NAME/KEY: VARIANT

140 &lt;222&gt; LOCATION: 69

141 &lt;223&gt; OTHER INFORMATION: Xaa = Any Amino Acid

143 &lt;400&gt; SEQUENCE: 2

144 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser

145 1 5 10 15

146 Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr

147 20 25 30

148 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser

149 35 40 45

150 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ala Ser

151 50 55 60

-&gt; 152 Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro

153 65 70 75 80

154 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val

155 85 90 95

156 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe

157 100 105 110

158 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser

159 115 120 125

160 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His

161 130 135 140

162 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys

163 145 150 155 160

164 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu

165 165 170 175

166 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu

167 180 185 190

168 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg

169 195 200 205

170 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu

171 210 215 220

172 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu

173 225 230 235 240

174 Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr

175 245 250 255

176 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr

177 260 265 270

178 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp

179 275 280 285

180 Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile

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Output Set: N:\CRF4\08292003\H572027C.raw

```

181      290      295      300
182 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
183 305      310      315      320
184 Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
185      325      330      335
186 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
187      340      345      350
188 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
189      355      360      365
190 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
191      370      375      380

```

193 &lt;210&gt; SEQ ID NO: 3

194 &lt;211&gt; LENGTH: 1155

195 &lt;212&gt; TYPE: DNA

196 &lt;213&gt; ORGANISM: Brassica napus

198 &lt;220&gt; FEATURE:

199 &lt;221&gt; NAME/KEY: CDS

200 &lt;222&gt; LOCATION: (1)...(1152)

201 <223> OTHER INFORMATION: Clone: IMC129, G to A transversion mutation at  
 202 nucleotide 316 of the D form

204 &lt;221&gt; NAME/KEY: misc\_feature

205 &lt;222&gt; LOCATION: 205

206 &lt;223&gt; OTHER INFORMATION: n = A,T,C or G

-&gt; 208 &lt;400&gt; 3

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209 atg ggt gca ggt gga aga atg caa gtg tct cct ccc tcc aag aag tct      48
210 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
211 1      5      10      15
213 gaa acc gac acc atc aag cgc gta ccc tgc gag aca ccg ccc ttc act      96
214 Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
215      20      25      30
217 gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc tcg      144
218 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
219      35      40      45
221 atc cct cgc tct ttc tcc tac ctc atc tgg gac atc ata gcc tcc      192
222 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ala Ser
223      50      55      60

```

-&gt; 225 tgc ttc tac tac ntc gcc acc act tac ttc cct ctc ctc cct cac cct 240

```

226 Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
227 65      70      75      80
229 ctc tcc tac ttc gcc tgg cct ctc tac tgg gcc tgc caa ggg tgc gtc      288
230 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
231      85      90      95
233 cta acc ggc gtc tgg gtc ata gcc cac aag tgc ggc cac cac gcc ttc      336
234 Leu Thr Gly Val Trp Val Ile Ala His Lys Cys Gly His His Ala Phe
235      100      105      110
237 agc gac tac cag tgg ctt gac gac acc gtc ggt ctc atc ttc cac tcc      384
238 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
239      115      120      125
241 ttc ctc ctc gtc cct tac ttc tcc tgg aag tac agt cat cgc agc cac      432

```

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Input Set : A:\07148-032001.txt

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242	Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Ser	His	
243		130					135					140					
245	cat	tcc	aac	act	ggc	tcc	ctc	gag	aga	gac	gaa	gtg	ttt	gtc	ccc	aag	480
246	His	Ser	Asn	Thr	Gly	Ser	Leu	Glu	Arg	Asp	Glu	Val	Phe	Val	Pro	Lys	
247	145					150					155					160	
249	aag	aag	tca	gac	atc	aag	tgg	tac	ggc	aag	tac	ctc	aac	aac	cct	ttg	528
250	Lys	Lys	Ser	Asp	Ile	Lys	Trp	Tyr	Gly	Lys	Tyr	Leu	Asn	Asn	Pro	Leu	
251					165					170						175	
253	gga	cg	acc	gtg	atg	tta	acg	gtt	cag	ttc	act	ctc	ggc	tgg	ccg	ttg	576
254	Gly	Arg	Thr	Val	Met	Leu	Thr	Val	Gln	Phe	Thr	Leu	Gly	Trp	Pro	Leu	
255				180					185					190			
257	tac	tta	gcc	ttc	aac	gtc	tcg	gga	aga	cct	tac	gac	ggc	ggc	ttc	cgt	624
258	Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Gly	Phe	Arg	
259			195					200					205				
261	tgc	cat	ttc	cac	ccc	aac	gct	ccc	atc	tac	aac	gac	cg	gag	cgt	ctc	672
262	Cys	His	Phe	His	Pro	Asn	Ala	Pro	Ile	Tyr	Asn	Asp	Arg	Glu	Arg	Leu	
263		210				215						220					
265	cag	ata	tac	atc	tcc	gac	gct	ggc	atc	ctc	gcc	gtc	tgc	tac	ggt	ctc	720
266	Gln	Ile	Tyr	Ile	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Tyr	Gly	Leu	
267	225				230					235						240	
269	ttc	cgt	tac	gcc	gcc	ggc	cag	gga	gtg	gcc	tcg	atg	gtc	tgc	ttc	tac	768
270	Phe	Arg	Tyr	Ala	Ala	Gly	Gln	Gly	Val	Ala	Ser	Met	Val	Cys	Phe	Tyr	
271				245						250					255		
273	gga	gtc	ccg	ctt	ctg	att	gtc	aat	ggt	ttc	ctc	gtg	ttg	atc	act	tac	816
274	Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Gly	Phe	Leu	Val	Leu	Ile	Thr	Tyr	
275				260						265					270		
277	ttg	cag	cac	acg	cat	cct	tcc	ctg	cct	cac	tac	gat	tcg	tcc	gag	tgg	864
278	Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp	
279			275					280					285				
281	gat	tgg	ttc	agg	gga	gct	ttg	gct	acc	gtt	gac	aga	gac	tac	gga	atc	912
282	Asp	Trp	Phe	Arg	Gly	Ala	Leu	Ala	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile	
283		290				295						300					
285	ttg	aac	aag	gtc	ttc	cac	aat	att	acc	gac	acg	cac	gtg	gcc	cat	cat	960
286	Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His	
287	305				310						315					320	
289	ccg	ttc	tcc	acg	atg	ccg	cat	tat	cac	gcg	atg	gaa	gct	acc	aag	gcg	1008
290	Pro	Phe	Ser	Thr	Met	Pro	His	Tyr	His	Ala	Met	Glu	Ala	Thr	Lys	Ala	
291				325						330					335		
293	ata	aag	ccg	ata	ctg	gga	gag	tat	tat	cag	ttc	gat	ggg	acg	ccg	gtg	1056
294	Ile	Lys	Pro	Ile	Leu	Gly	Glu	Tyr	Tyr	Gln	Phe	Asp	Gly	Thr	Pro	Val	
295				340						345				350			
297	gtt	aag	gcg	atg	tgg	agg	gag	gcg	aag	gag	tgt	atc	tat	gtg	gaa	ccg	1104
298	Val	Lys	Ala	Met	Trp	Arg	Glu	Ala	Lys	Glu	Cys	Ile	Tyr	Val	Glu	Pro	
299			355					360					365				
301	gac	agg	caa	ggt	gag	aag	aaa	ggt	gtg	ttc	tgg	tac	aac	aat	aag	tta	1152
302	Asp	Arg	Gln	Gly	Glu	Lys	Lys	Gly	Val	Phe	Trp	Tyr	Asn	Asn	Lys	Leu	
303		370				375						380					
305	tga																1155
307	<210> SEQ ID NO: 4																

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/08/572,027C

DATE: 08/29/2003  
TIME: 15:01:29

Input Set : A:\07148-032001.txt  
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ease Note:

e of n and/or Xaa have been detected in the Sequence Listing. Please review the  
quence Listing to ensure that a corresponding explanation is presented in the <220>  
<223> fields of each sequence which presents at least one n or Xaa.

q#:1; N Pos. 205  
q#:1; Xaa Pos. 69  
q#:2; Xaa Pos. 69  
q#:3; N Pos. 205  
q#:3; Xaa Pos. 69  
q#:4; Xaa Pos. 69